CLAIMS AMENDMENTS

Claims 1-8 (canceled).

Claim 9 (new): A method for identifying at least one mutation and/or polymorphism that is a major determinant of a phenotype, comprising calculating a residual deviance (δ) of a predetermined group of mutations and/or polymorphisms identified within a gene.

Claim 10 (new): The method according to claim 9, wherein the residual deviance (δ) is calculated for each possible subset of said predetermined group of mutations and/or polymorphisms.

Claim 11 (new): The method according to claim 10, wherein said each possible subset of mutations and/or polymorphisms is defined by partitioning a predetermined group of haplotypes {1...m} corresponding to said mutations and/or polymorphisms.

Claim 12 (new): The method according to claim 11, wherein the residual deviance (δ) is calculated as $\delta = \delta(\Pi) = \sum_{i=1}^{m} (\chi_i - \bar{\chi}_{\pi(i)})^2$.

Claim 13 (new): A method for predicting a super-maximal and/or a sub-minimal haplotype that are major determinants of a corresponding super-maximal

phenotype and a sub-minimal phenotype, comprising calculating a residual deviance (δ) of said super-maximal and/or sub-minimal haplotype in accordance with the method of claim 11.

Claim 14 (new): A method for identifying at least one single nucleotide polymorphism (SNP) that is of phenotypic significance, comprising calculating a residual deviance (δ) of said at least one single nucleotide polymorphism (SNP) in accordance with the method of claim 11.

Claim 15 (new): A detection method for detecting a haplotype effective to act as an indicator of at least one phenotype in an individual, which detection method comprises the steps of:

(a) obtaining a test sample of genetic material from an individual to be tested, said material comprising at least a selected gene or a fragment thereof;

(b) analysing a nucleotide sequence of said gene or fragment thereof to determine whether single nucleotide polymorphisms (SNPs) exist at any one or more of the SNP sites within the gene; and

(c) where said SNPs exist, identifying them in order to determine a haplotype of said individual; and

(d) calculating a residual deviance (δ) of said haplotype in accordance with the method of claim 11.

Claim 16 (new): A method for identifying a haplotype which is phenotypically significant in the diagnosis or treatment of a disease characterised by said phenotype, comprising calculating a residual deviance (δ) of said haplotype in accordance with the method of claim 11.